RAW SEQUENCE LISTING   DATE: 03/13/2001
PATENT APPLICATION: US/09/274,752C   TIME: 17:08:17

Input Set : A:\A-67501.app
Output Set: N:\CRF3\03132001\I274752C.raw

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 3  <110> APPLICANT: Goetzl, Edward L.
 4        An, Songzhu
 6  <120> TITLE OF INVENTION: Human Polypeptide Receptors for Lysophospholipids and
 7        Sphingolipids and Nucleic Acids Encoding the Same
 9  <130> FILE REFERENCE: A-67501/DJB/TAL
11  <140> CURRENT APPLICATION NUMBER: 09/274,752C
12  <141> CURRENT FILING DATE: 1999-03-23
14  <160> NUMBER OF SEQ ID NOS: 29
16  <170> SOFTWARE: PatentIn Ver. 2.0
18  <210> SEQ ID NO: 1
19  <211> LENGTH: 382
20  <212> TYPE: PRT
21  <213> ORGANISM: Homo sapiens
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27  Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
28              20                  25                  30
30  Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
31          35                  40                  45
33  Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
34      50                  55                  60
36  Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
37  65                  70                  75                  80
39  Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
40              85                  90                  95
42  Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
43              100                 105                 110
45  Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
46          115                 120                 125
48  Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
49      130                 135                 140
51  Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
52  145                 150                 155                 160
54  Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp
55              165                 170                 175
57  Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
58              180                 185                 190
60  Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
61          195                 200                 205
63  Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
64      210                 215                 220
66  His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
67  225                 230                 235                 240
69  Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
70              245                 250                 255
72  Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
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73            260              265              270
75 Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
76         275              280              285
78 Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ser Glu Met Arg Arg
79         290              295              300
81 Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
82 305              310              315              320
84 Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
85              325              330              335
87 Ile Met Leu Pro Glu Asn Gly His Pro Leu Met Thr Pro Pro Phe Ser
88         340              345              350
90 Tyr Leu Glu Leu Gln Arg Tyr Ala Ala Ser Asn Lys Ser Thr Ala Pro
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93 Asp Asp Leu Trp Val Leu Leu Ala Gln Pro Asn Gln Gln Asp
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98 <211> LENGTH: 1734
99 <212> TYPE: DNA
100 <213> ORGANISM: Homo sapiens
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105 atcggcttct tctataacaa cagtggcaaa gagctcagct cccactggcg gcccaaggat 180
106 gtggtcgtgg tggcactggg gctgaccgtc agcgtgctgg tgctgctgac caatctgctg 240
107 gtcatagcag ccatcgcctc caaccgccgc ttccaccagc ccatctacta cctgctcggc 300
108 aatctggccg cggctgacct cttcgcgggc gtggcctacc tcttcctcat gttccacact 360
109 ggtccccgca cagcccgact ttcacttgag ggctggttcc tgcggcaggg cttgctggac 420
110 acaagcctca ctgcgtcggt ggccacactg ctggccatcg ccgtggagct gcaccgcagt 480
111 gtgatgtccg tgcagctgca cagccgcctg ccccgtggcc gcgtggtcat gctcattgtg 540
112 ggcgtgtggg tggctgccct gggcctgggg ctgctgcctg cccactcctg gcactgcctc 600
113 tgtgccctgg accgctgctc acgcatggca cccctgctca gccgctccta tttggccgtc 660
114 tgggctctgt cgagcctgtc tgtcttcctg ctcatggtgg ctgtgtacac ccgcattttc 720
115 ttctacgtgc ggcggcgagt gcagcgcatg gcagagcatg tcagctgcca ccccgctac 780
116 cgagagacca cgctcagcct ggtcaagact gttgtcatca tcctgggggc gttcgtggtc 840
117 tgctggacac caggccaggt ggtactgctc ctggatggtt taggctgtga gtcctgcaat 900
118 gtcctggctg tagaaaagta cttcctactg ttggccgagg ccaactcact ggtcaatgct 960
119 gctgtgtact cttgccgaga tgctgagatg cgccgcacct tccgccgcct tctctgctgc 1020
120 gcgtgcctcc gccagtccac ccgcgagtct gtccactata catcctctgc ccagggaggt 1080
121 gccagcactc gcatcatgct tcccgagaac ggccacccac tgatgactcc accctttagc 1140
122 taccttgaac ttcagcggta cgcggcaagc aacaaatcca gcccctga tgacttgtgg 1200
123 gtgctcctgg ctcaacccaa ccaacaggac tgactgactg gcaggacaag gtctggcatg 1260
124 gcacagcacc actgccaggc ctccccaggc acaccactct gcccagggaa tgggggcttt 1320
125 gggtcatctc ccactgcctg ggggagtcag atggggtgca ggaatctggc tcttcagcca 1380
126 tctcaggttt aggggtttg taacagacat tattctgttt tcactgcgta tccttggtaa 1440
127 gccctgtgga ctggttaatg ctgtgtgatg ctgagggttt taaggtgggg agagataagg 1500
128 gctctctcgg gccatgctac ccggtatgac tgggtaatga ggacagactg tggacacccc 1560
129 atctacctga gtctgattct ttagcagcag agactgaggg gtgcagagtg tgagctggga 1620
130 aaggtttgtg gctccttgca gcctccaggg actggcctgt ccccaataga attgaagcag 1680
131 tccacgggga ggggatgata caaggagtaa acctttcttt acactcaaaa aaaa 1734
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Input Set : A:\A-67501.app
Output Set: N:\CRF3\03132001\I274752C.raw

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134 <211> LENGTH: 353
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 3
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140  1               5                  10                  15
142 His Tyr Asn Tyr Thr Lys Glu Thr Leu Glu Thr Gln Glu Thr Thr Ser
143              20                  25                  30
145 Arg Gln Val Ala Ser Ala Gly Ile Val Ile Leu Cys Cys Ala Ile Val
146          35                  40                  45
148 Val Glu Asn Leu Leu Val Leu Ile Ala Val Ala Arg Asn Ser Lys Phe
149      50                  55                  60
151 His Ser Ala Met Tyr Leu Phe Leu Gly Asn Leu Ala Ala Ser Asp Leu
152  65                  70                  75                  80
154 Leu Ala Gly Val Ala Phe Val Ala Asn Thr Leu Leu Ser Gly Ser Val
155              85                  90                  95
157 Thr Leu Arg Leu Thr Pro Val Gln Trp Phe Ala Arg Glu Gly Ser Ala
158          100                 105                 110
160 Ser Ile Thr Leu Ser Ala Ser Val Gly Ser Leu Leu Ala Ile Ala Ile
161          115                 120                 125
163 Glu Arg His Val Ala Ile Ala Lys Val Lys Leu Tyr Gly Ser Cys Lys
164          130                 135                 140
166 Ser Cys Arg Met Leu Leu Leu Ile Gly Ala Ser Trp Leu Ile Ser Leu
167 145                 150                 155                 160
169 Val Leu Gly Gly Leu Pro Ile Leu Gly Trp Asn Cys Leu Gly His Leu
170              165                 170                 175
172 Glu Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys His Tyr Val Leu
173              180                 185                 190
175 Cys Val Val Thr Ile Phe Ser Ile Ile Leu Leu Ala Ile Val Ala Leu
176          195                 200                 205
178 Tyr Val Arg Ile Tyr Cys Val Val Arg Ser Ser His Ala Asp Met Ala
179      210                 215                 220
181 Ala Pro Gln Thr Leu Ala Leu Leu Lys Thr Val Thr Ile Val Leu Gly
182 225                 230                 235                 240
184 Val Phe Ile Val Cys Trp Leu Pro Ala Phe Ser Ile Leu Leu Leu Asp
185              245                 250                 255
187 Tyr Ala Cys Pro Val His Ser Cys Pro Ile Leu Tyr Lys Ala His Tyr
188          260                 265                 270
190 Phe Phe Ala Val Ser Thr Leu Asn Ser Leu Leu Asn Pro Val Ile Tyr
191          275                 280                 285
193 Thr Trp Arg Ser Arg Asp Leu Arg Arg Glu Val Leu Arg Pro Leu Gln
194          290                 295                 300
196 Cys Trp Arg Pro Gly Val Gly Val Gln Gly Arg Arg Arg Val Gly Thr
197 305                 310                 315                 320
199 Pro Gly His His Leu Leu Pro Leu Arg Ser Ser Ser Ser Leu Glu Arg
200              325                 330                 335
202 Gly Met His Met Pro Thr Ser Pro Thr Phe Leu Glu Gly Asn Thr Val
203              340                 345                 350
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Input Set : A:\A-67501.app
Output Set: N:\CRF3\03132001\I274752C.raw

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205 Val
209 <210> SEQ ID NO: 4
210 <211> LENGTH: 1122
211 <212> TYPE: DNA
212 <213> ORGANISM: Homo sapiens
214 <400> SEQUENCE: 4
215 atgggcagct tgtactcgga gtacctgaac cccaacaagg tccaggaaca ctataattat 60
216 accaaggaga cgctggaaac gcaggagacg acctcccgcc aggtggcctc ggccttcatc 120
217 gtcatcctct gttgcgccat gcaggagacg acctcccgcc aggtggcctc ggccttcatc 180
218 gtcatcctct gttgcgccat tgtggtggaa aaccttctgg tgctcattgc ggtggcccga 240
219 aacagcaagt tccactcggc aatgtacctg tttctgggca acctggccgc ctccgatcta 300
220 ctggcaggcg tggccttcgt agccaatadd ttgctctctg gctctgtcac gctgaggctg 360
221 acgcctgtgc agtggtttgc ccgggagggc tctgcctcca tcacgctctc ggcctctgtc 420
222 ttcagcctcc tggccatcgc cattgagcgc cacgtggcca ttgccaaggt caagctgtat 480
223 ggcagcgaca agagctgccg catgcttctg ctcatcgggg cctcgtggct catctcgctg 540
224 gtcctcggtg gcctgcccat ccttggctgg aactgcctgg gccacctcga ggcctgctcc 600
225 actgtcctgc ctctctacgc caagcattat gtgctgtgcg tggtgaccat cttctccatc 660
226 atcctgttgg ccatcgtggc cctgtacgtg cgcatctact gcgtggtccg ctcaagccac 720
227 gctgacatgg ccgccccgca gacgctagcc ctgctcaaga cggtcaccat cgtgctaggc 780
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230 tccctgctca accccgtcat ctacacgtgg cgcagccggg acctgcggcg ggaggtgctt 960
231 cggccgctgc agtgctggcg gccggggggtg ggggtgcaag gacggaggcg ggtcgggacc 1020
232 ccgggccacc acctcctgcc actccgcagc tccagctccc tggagagggg catgcacatg 1080
233 cccacgtcac ccacgtttct ggagggcaac acggtggtct ga                  1122
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236 <211> LENGTH: 375
237 <212> TYPE: DNA
238 <213> ORGANISM: Homo sapiens
240 <400> SEQUENCE: 5
241 gggccatggc tcgagccgcc ccgacccccc gcgagcccgc cttgtctgcg gcgtgactgg 60
242 aggcccagat ggtcatcatg ggccagtgct actacaacga gaccatcggc ttcttctata 120
243 acaacagtgg caaagagctc agctcccact ggcggcccaa ggatgtggtc gtggtggcac 180
244 tggggctgac cgtcagcgtg ctggtgctgc tgaccaatct gctggtcata gcagccatcg 240
245 cctccaaccg ccgcttccac cagcccatct actacctgct cggcaatctg gccgcggctg 300
246 acctcttcgc gggcgtggct acctcttcct catgttccac actggtcccc gcacagcccg 360
247 actttcactt gaggg                                                375
249 <210> SEQ ID NO: 6
250 <211> LENGTH: 8
251 <212> TYPE: PRT
252 <213> ORGANISM: combination of rat and human.
254 <400> SEQUENCE: 6
255 Leu Leu Ala Ile Ala Ile Glu Arg
256   1               5
259 <210> SEQ ID NO: 7
260 <211> LENGTH: 22
261 <212> TYPE: DNA
262 <213> ORGANISM: combination of rat and human.
264 <220> FEATURE:
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Input Set : A:\A-67501.app
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```
265 <221> NAME/KEY: misc_feature
266 <222> LOCATION: (6)
267 <223> OTHER INFORMATION: The n at position 6 can be g or c.
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (12)
272 <223> OTHER INFORMATION: The n at position 12 can be c or t.
274 <220> FEATURE:
275 <221> NAME/KEY: misc_feature
276 <222> LOCATION: (17)
277 <223> OTHER INFORMATION: The n at position 17 can be c or t.
279 <220> FEATURE:
280 <221> NAME/KEY: misc_feature
281 <222> LOCATION: (21)
282 <223> OTHER INFORMATION: The n at position 21 can be a or c.
284 <400> SEQUENCE: 7
285 ctcctngcca tngcatngag ng                              22
287 <210> SEQ ID NO: 8
288 <211> LENGTH: 8
289 <212> TYPE: PRT
290 <213> ORGANISM: combination of rat and human.
292 <400> SEQUENCE: 8
293 Leu Leu Leu Leu Asp Ser Thr Cys
294   1               5
297 <210> SEQ ID NO: 9
298 <211> LENGTH: 22
299 <212> TYPE: DNA
300 <213> ORGANISM: combination of rat and human.
302 <220> FEATURE:
303 <221> NAME/KEY: misc_feature
304 <222> LOCATION: (4), (15), (21)
305 <223> OTHER INFORMATION: The n at position 4, 16, and 22 can be c or g.
307 <220> FEATURE:
308 <221> NAME/KEY: misc_feature
309 <222> LOCATION: (6), (8)
310 <223> OTHER INFORMATION: The n at position 6 and 8 can be a or c.
312 <220> FEATURE:
313 <221> NAME/KEY: misc_feature
314 <222> LOCATION: (7), (9), (18)
315 <223> OTHER INFORMATION: The n at position 7, 9, and 19 can be a or g.
317 <400> SEQUENCE: 9
318 cagntnnnt ccagnagnag na                               22
320 <210> SEQ ID NO: 10
321 <211> LENGTH: 24
322 <212> TYPE: DNA
323 <213> ORGANISM: Homo sapiens
325 <400> SEQUENCE: 10
326 gcaggacagt ggagcaggcc tcga                            24
328 <210> SEQ ID NO: 11
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VERIFICATION SUMMARY   DATE: 03/13/2001
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Input Set : A:\A-67501.app
Output Set: N:\CRF3\03132001\I274752C.raw

L:285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9